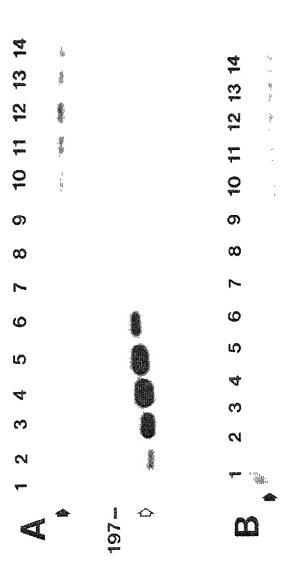
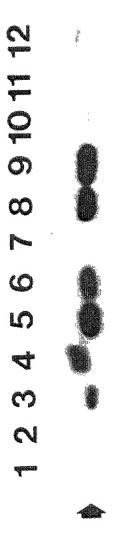
Figure 1



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Figure 2



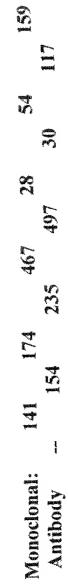


Figure 3

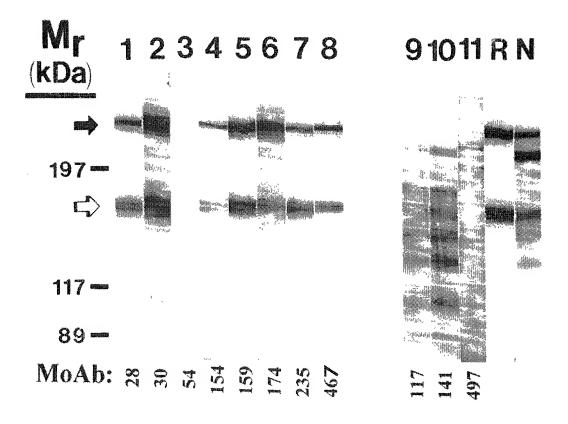
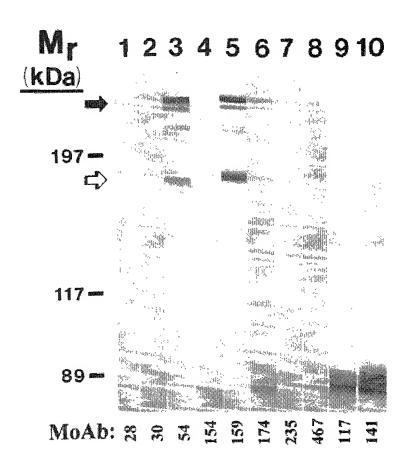
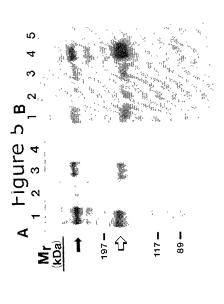


Figure 4





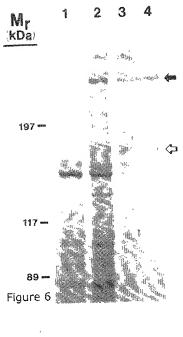
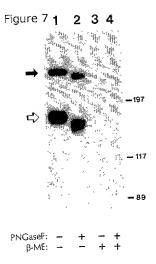


Figure 6

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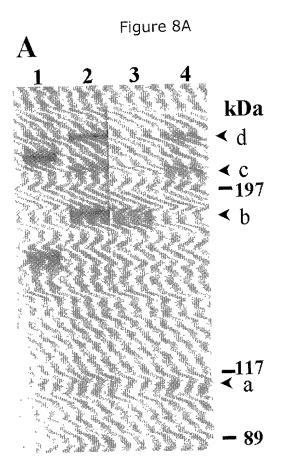
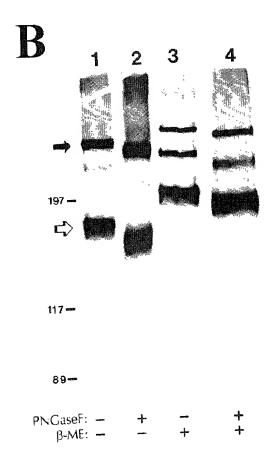
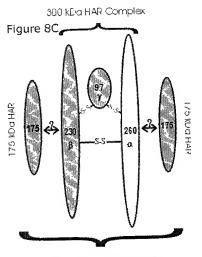


Figure 8B





Super-large HAR Complex

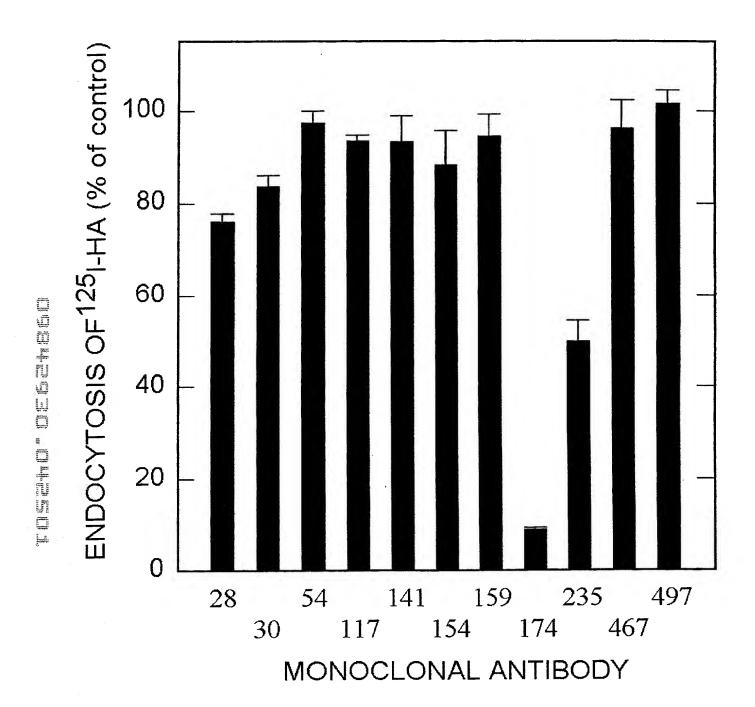
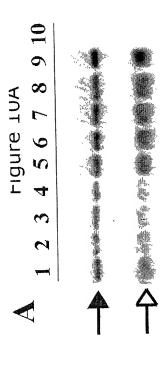


Figure 9



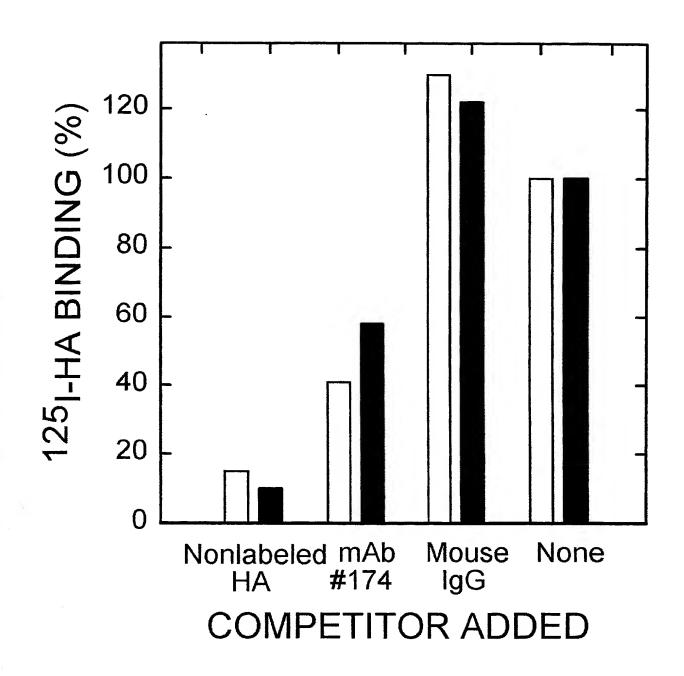


Figure 10B

Figure 11

Antibody Inhibition of HA Endocytosis by HARE in LECs

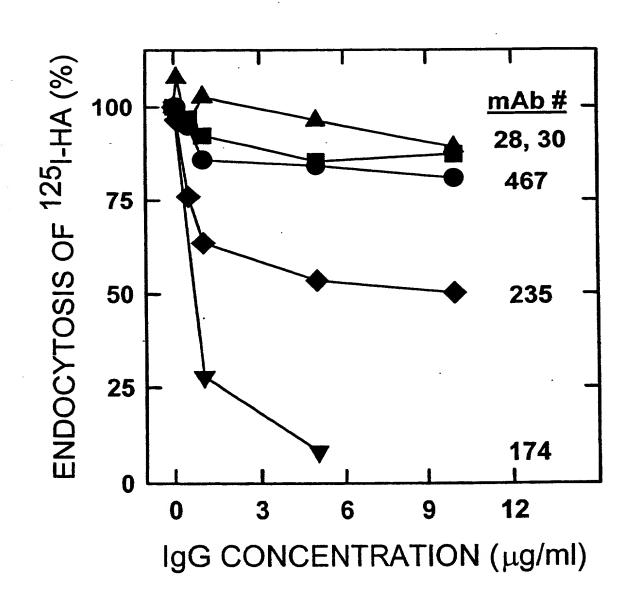
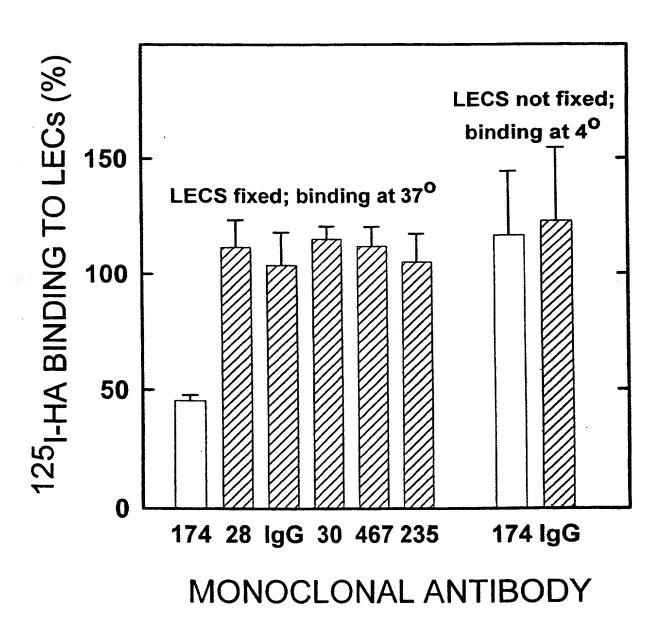
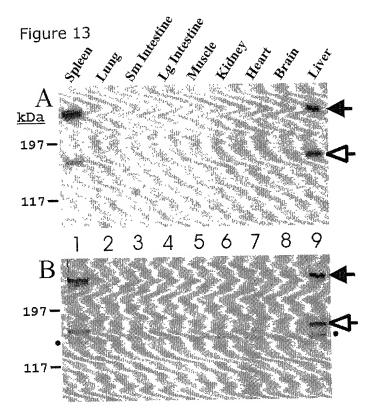
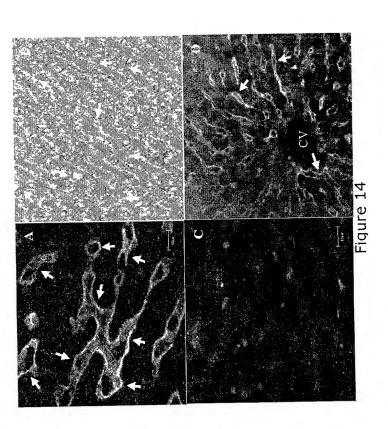


Figure 12

Antibody Inhibition of HA Binding to HARE on LECs is Temperature Dependent







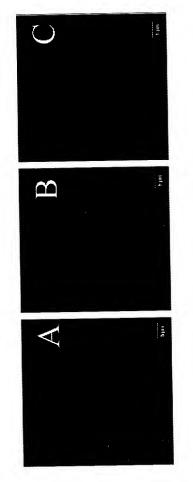
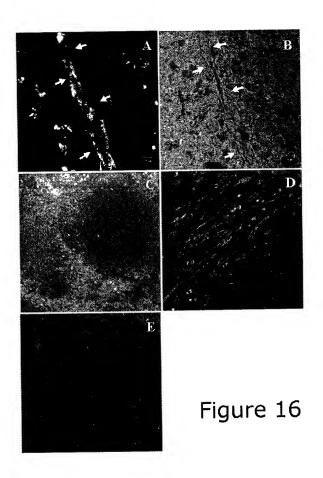


Figure 15



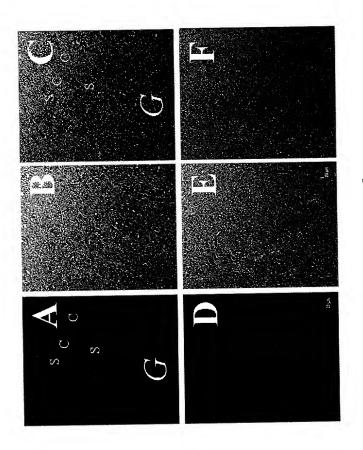
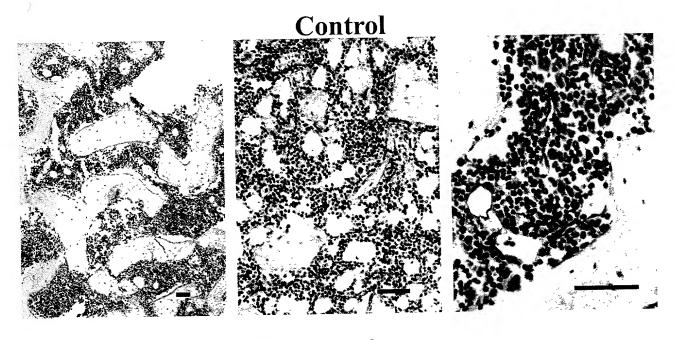


Figure 17

Immunolocalization of HARE in Bone Marrow



Bars = 50 um

Figure 19

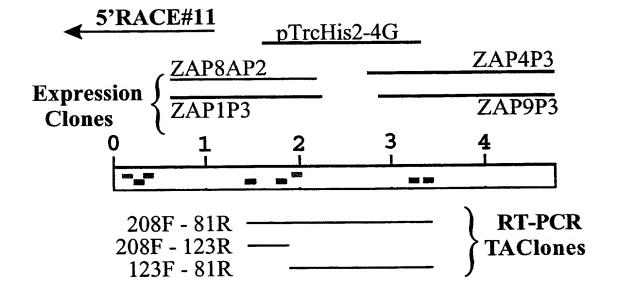
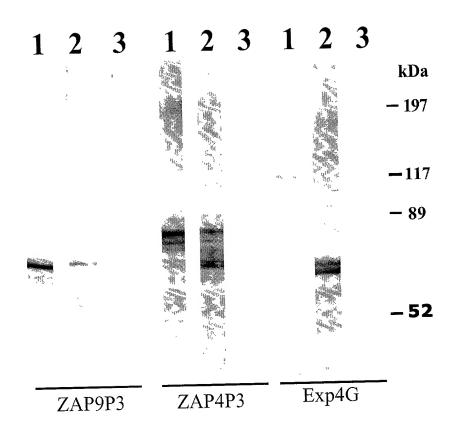


Figure 20



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41 V P N N E A I E N Y I R E K K A T S L K E D I L R Y H V V L G E K L L K N D L H
361 GGAGTGATCCATGGTCTGGAGAAGTTCTGGAAAATTCAGAAGAACAGATGTGACAATAATGACACCATTATTGTGAGAGGGGAGTGTGGAAAGTGTTCCCAGCAAGCCCCCTGCCCACTC 121 \underline{G} \underline{V} \underline{I} \underline{H} \underline{G} \underline{L} \underline{E} \underline{K} \underline{V} \underline{L} \underline{E} \underline{I} \underline{Q} \underline{K} \underline{N} \underline{R} \underline{C} \underline{D} \underline{N} \underline{N} \underline{D} \underline{T} \underline{I} \underline{I} \underline{V} \underline{R} \underline{G} \underline{E} \underline{C} \underline{G} \underline{K} \underline{C} \underline{C}
961 AAATGTGCGGCAGGATTCCGAGGGAATGGAACGGTCTGCACAGCCATCAATGCCTGTGAGACCAGCAATGGAGGATGTTCTACAAAGGCCGACTGTAAAAGAACCACCCCAGGAAACCGG 321 K C A A G F R G N G T V C T A I N A C E T S N G G C S T K A D C K R T T P G N R
201 CAGGCCGTCTGTAACTGCTTGCCGAAGTACACTGGAGATAGGTCTGCTCGCTTATCAATGTCTGCCCTAACGAACAATGGCGGCTGCAGTCCATTTGCCTTCTGCAACTACACTGAG
401 Q A V C N C L P K Y T G D G K V C S L I N V C L T N N G G C S P F A F C N Y T E
321 CAAGATCAAAGGATATGTACCTGCAGGCCAGACTACACGGGTGATGGAATCGTCTGCCGGGGCAGCATCTACGGGGAGCTTCCCAAGAACCCTTCGACGTACCTCCTCCAGTACTTCTTCCAGTTG 441 Q D Q R I C T C K P D Y T G D G I V C R G S I Y G E L P K N P S T S Q Y F F Q L
SE1 CAGGTTCTTCGCTATCACGTGGTGGGCTGCCAGCAGCTGCTGTTGGACAACCTAAAAGTGACCACAAGTGCCACGACCCTCCAAGGAGAGCCAGTTTCCATCTCTGTCTCTCAGGACACT

5⊋1 Q V L R Y H V V G C Q Q L L L D N L K V T T S A T T L Q G E P V S I S V S Q D T
_281 GATATTCCGGGGGGGGGGGGGGGAGTTGCATTTCACTCCCAAATGCCCACTGAAGAGCCAAGCCAAAGGGGGTGAAGAAGAGTGTATCTACAACCCGTTACCTTTCAGGAGGAACGTGGAA
4D1 GGCTGCCAGAACCTGTGCACCGTGGTGATCCAAACCCCCAGGTGCTGCCATGGTTACTTCATGCCAGACTGTCAGGCCTGCCCTGGAGGACCAGATACACCGTGTAACAACCGGGGCATG
BA1 G C Q N L C T V V I Q T P R C C H G Y F M P D C Q A C P G G P D T P C N N R G M
TS21 TGCCGCGATCTGTACACACCCATGGGACAGTGCCTATGCCACACCGGCTTCAACGGGACAGCCTGCGGAGCTCTGCTGGCATGGGAGATTTGGGCCTGACTGTCAGCCCCGCAGCTGCTCC
T821 C R D L Y T P M G Q C L C H T G F N G T A C E L C W H G R F G P D C Q P R S C S
GAL GAGCATGGACAGTGTGATGAGGGGATCACAGGCTCCGGGGAGTGCCTCTGTGAAACAGGGTGGACAGCCGCTTCGTGTGACACTCCCACAGCTGTATTCGCAGTGTGCACACCTGCTTGC

BBL E H G Q C D E G I T G S G E C L C E T G W T A A S C D T P T A V F A V C T P A C
881 GTCGCTAAGTGCTCCCAGAAAGGCACCCAAGTCTCTTGCAGCTGCAAGAAAGGCTACAAGGGGGATGGCTACAGCTGCATAGAGATAGACCCCTGTGCAGACGGTGTCAACGGGGGATGC
961 V A K C S O K G T O V S C S C K K G Y K G D G Y S C I E I D P C A D G V N G G C
 121 CAGGACAACGGACAGTGCCACCCAGATGCCAGCTGTGCAGACCTTACTTCCAGGACACGACCGTAGGAGTATTCCATCTACGCTCCCCACTGGGCCAGTACAAACTGACATTTGACAAA
041 Q D N G Q C H P D A S C A D L Y F Q D T T V G V F H L R S P L G Q Y K L T F D K
 841 CAAGAGACCAGGTTTGTGGATGGAAGATCCATTCTGCAGTGGGACATCATCGCCGCCAATGGAATCCTCCCATATTATTTCTGAACCTTTGAGAGCTCCTCCCACGGCAGCAACGGCTGCC 281 Q E T R F V D G R S I L Q W D I I A A N G I L H I I S E P L R A P P T A A T A A
 961 CACTCTGGCCTGGGGACAGGTATATTCTGTGCCGTCGTCGTCACTGGTGCGATTGCTCTGGCAGCTTACTCTTACTTCCGGCTAAGCAGCGAACCACTGGTTTCCAGCGTTTTGAT
321 H S G L G T G I F C A V V L V T G A I A L A A S S L B R K Q R T T G
 081 CAGAAGAGGACATTGATGTCTTGGCAGCAGCAGCAGCAGCACCAAGAATATCGCAAAACCCTCTGTATGAGACCTCAGCGCCGCACCCCCAGAGTCCTCCTGTGACCCCTTCACAGACC
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Figure 22

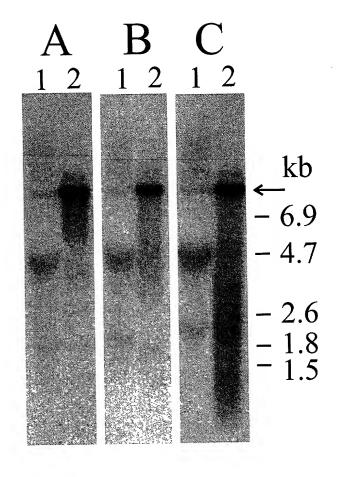


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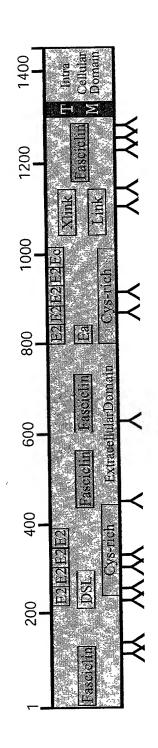
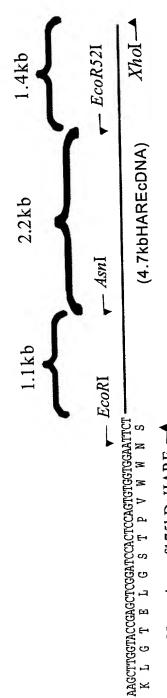


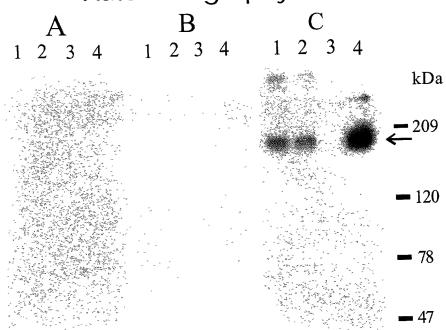
Figure 24

SignalCleavage Site ─▲ - Ig-kappachainLeaderSequence Nhel 📥



N-terminus of 175kDaHARE

Autoradiography



Western Blot

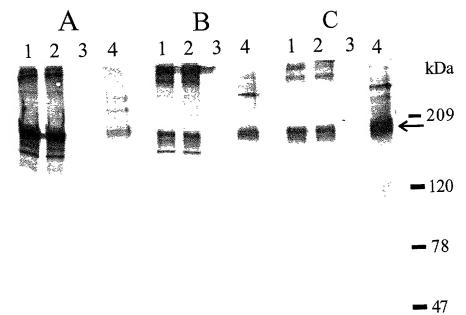


Figure 26

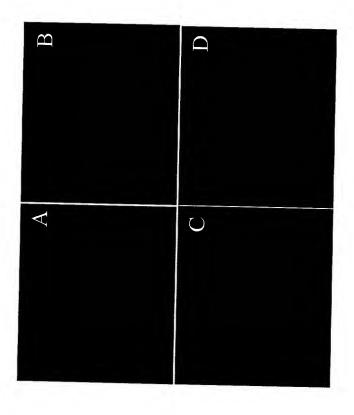
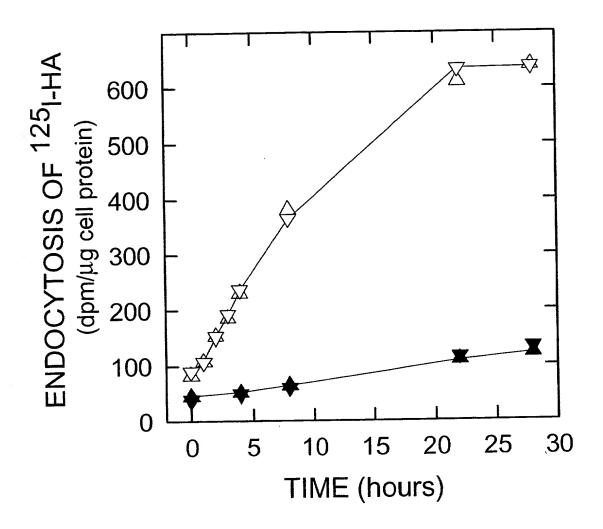


Figure 27A



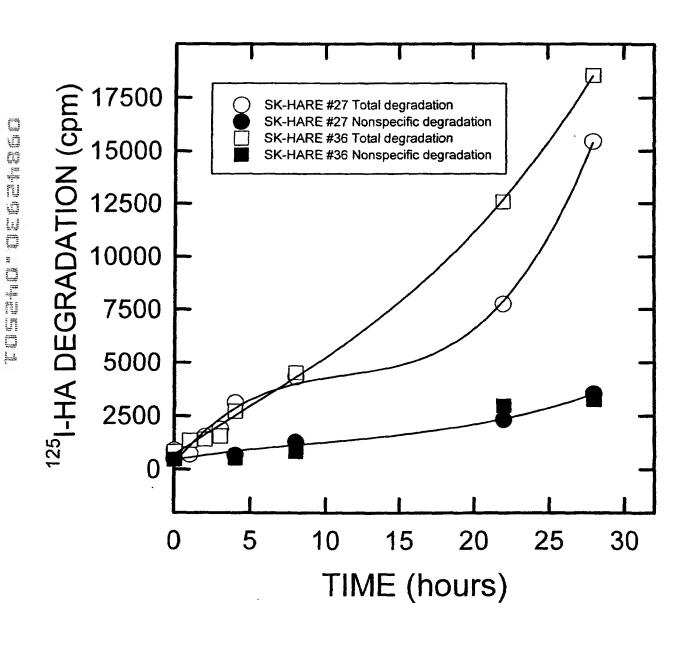
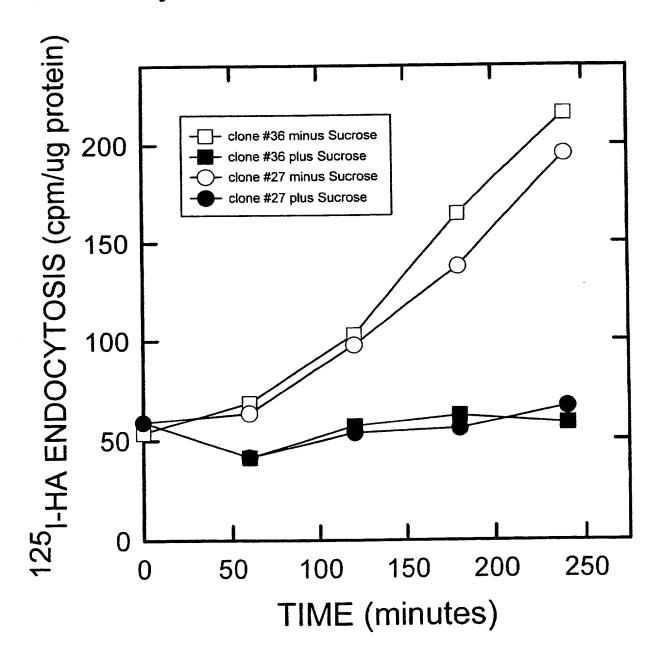
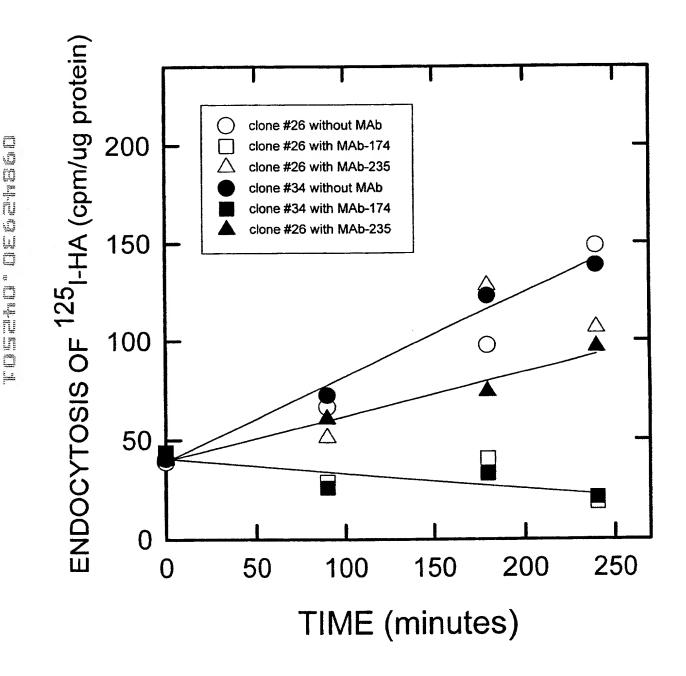


Figure 27C

Hyperosmolarity inhibits HA endocytosis mediated by HARE in transfected SK-Hep1 cells





			_	•								
	175HARE CAB61827 BAA13377	1 1111 LHILSQVLI 754 LHILSQVLI		LLQQLDLVPA	FSLFRELLQH	HGLVPQIEAA	TAYTIFVPTN	RSLEAQG	NSSHLDADTV	RHHVVLGEAL	SMETLR KGGH	RNSLLGPAHW
	175HARE CAB61827 BAA13377	95 LAFFLRND 1218 IVFYNHSO 861 IVFYNHSO	L YVNEAPINYT P EVNHVPLEGP P EVNHVPLEGP	MLEAPGRSLI	GLSGVLTVGS	SRELHSHAEA	LREKVNITR	RFRETQGFQL	QDTPRKS	RSGFSFSR	~-GSYTAK	KIQVPD CPG
	175HARE BAB15793 CAB61358	204 SLAHNAKPA 1 1	P GEVK-MEALG	TASVWDGVNG HLFGWSDG	TGT O GLGF TGV E GEGF	ngta et te sgta et te	GKYGIH DQA GKYGIH DQA	SVHGR SQ SVHGR NQ	GPLGDGS D GPLGDGS D	DVGWRGVK D DVGWRGVH D	MEITTON NG NATTEDN NG	T HTSAN LL T HTSAN LT VG
	CAB61827 BAA13377	1224 FFGTLCEPO 967 FFGTLCEPO	P GGLGGVES-G P GGLGGVES-G	HGQCQDRFLG HGQCQDRFLG	SGE HEHEGF SGE HEHEGF	hgta ev el hgta ev el	GRYGPN TGV GRYGPN TGV	DEAHGLEQE DEAHGLEQE	GLQGDGS V	NVGWQGLR D NVGWQGLR D	QKITSPQ PR QKITSPQ PR	k dpnan vq k dpnan vq
	175HARE BAB15793 CAB61358	313 DPDGKAS P 90 NSDGTAS P 3 EAVGTAS P	AAGFQGNGTI AAGFOGNGTI	TAINAEIS	NGGESAKAD	KRTTPGRRV	TEKAGYTGDG	IVELEINPEL	ENHGC DKNA	ETOTGPNOA	A N LPAYTG	DG-KV TLIN
	CAB61827 BAA13377	1433 DSAGAST A 1076 DSAGAST A	AAGYSGNGIF AAGYSGNGIF	SEVDP AHG SEVDP AHG	HGG SPHAN	TKVAPGQRT	TEQDGYMGDG	EL QEINS L	IHHGGHIHA	EFIPTGPQQV	SESEREGYSG	DGIRT
	175HARE BAB15793 CAB61358	422 V LINNGG 199 V LIKNGG 112 V LIKNGG	s pfafenyteq s efaienhtgq s efaienhtgq	DQRI T KPD VERT T KPN VERT T KPN	Y-IGDGFT R	GSIYQELPKN	PKTSQYFFQL	QEHFV KDLVG	PGPFTVFAP-	LSAAFDEE	ARVKDWDKYG	TWEGATKAHA
	AAF82398 CAB61827 BAA13377	1 1543 P SKNNGG 1186 P SKNNGG	S PVATEKSTGD	CORTETEDTA	HTVGDGL/T#R	ARVGLELLRD	KHASFFSL	RLLEYKELKG	DGPFTIFVPH	ADLMSNLSOD	ELARIRAHRO	-MPQVLRYHV LVFRYHV
	175HARE BAB15793	528 VG QQLLLI 305 VA HQLLLI	N LKLISNATSL	QGEPIVISVS	QSTVYINNKA	KIISSDIIST	NGIVHIIDKL	LSPKNLLITP	KDNSGRILQN	LTTLATINGY	IKFSNLIQDS	GLLSVITDPI
	CAB61358 AAF82398 CAB61827	1648 VG RRLRSE	N LKLISNATSL D LLEOGYATAL	QGEPIVISVS SGHPLRFSER	QSTVYINNKA EGSIYLNDFA	KI ISSDIIST RVVSSDHEAV	NGIVHIIDKL NGILHFIDRV	LSPKNLLITP LLPPEALHWE	KDNSGRILQN PDDAPIPRRN	LTTLATNNGY VTAAAQGFGY	IKFSNLIQDS KIFSGLLKVA	GLLSVITDPI GLLPLLREAS
the state of the s	BAA13377	1291 VG RRLRSE	D LLEQGYATAL	SGHPLRFSER	EGSIYLNDFA	RVVSSDHEAV	NGILHFIDRV	LLPPEALHWE	PDDAPIPRRN	VTAAAQGFGY	K IFSGLLKVA	GLLPLLREAS
	175HARE BAB15793 CAB61358	415 HTPVTLFWI 328 HTPVTLFWI	T DQALHALPAE T DQALHALPAE	QQDFLFNQDN QQDFLFNQDN	KDKLKEYLKF KDKLKEYLKF	HVIRDAKVLA HVIRDAKVLA	VDLPTSTAWK VDLPTSTAWK	TLQGSELSVK TLQGSELSVK	GAGRDIGDL GAGRDIGDL	FLNGQT RIV FLNGQT RIV	QRELLFDLGV QRELLFDLGV	AYGID LLID
	AAF82398 CAB61827 BAA13377	120 HTPVTLFWI 1758 HRPFTMLWI 1401 HRPFTMLWI	T DAAFRALPPD	ROAWLYHEDH	RDKLAAILRG	HMIRNVEALA	SDLPNLGPLR	TMHGTPISFS	SRTRP-GEL	MVGEDDARIV	QRHLPF EGGL	AYGIDQLLEP
	175HARE BAB15793	748 PTLGGR D. 525 PTLGGR D.	F TTFDAS-GE	GS VNTPS P	RWSKPKGVKQ	K LY	N-LPF	K	RNLE-G	RER SLVIQI	PRKGYFGR	D QA PGGPD
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	BAA13377	1510 PGLGAR DI	IF ETRPLRLNT	SIGLEPPPP	EGSQEQGSPE	AWRFYPKFW	TSPPLHSLGL	RSVWVHPSLW	GRPQGLGRG	HRN	PGHYGS	E QA PGGPS
	175HARE BAB15793 CAB61358	609 AP NINRGV 522 AP NINRGV	L DQYSATGE K L DQYSATGE K	ntgfngta ntgfngta	EM WPGRFGP EM WPGRFGP	D LPCG SDH D LPCG SDH	GO DDGITGS GO DDGITGS	GQ L ETGWT GQ L ETGWT	GPS DTQAVL GPS DTQAVL	PAV TPP SA PAV TPP SA	HAT KENNT HAT KENNT	E NLDYEGDG E NLDYEGDG
	AAF82398 CAB61827 BAA13377	833 TP NNRGM 609 AP NNRGV 522 AP NNRGV 314 AP NNRGV 1977 SP SDRGV 1620 SP SDRGV	L DQYSATGE K M DGMSGSGQ L M DGMSGSGQ L	ntgfngta RSG fagta RSG fagta	EL APGAFGP EL APGAFGP	H QACR TVH H QACR TVH	GR DEGLGGS GR DEGLGGS	GS F DEGWT GS F DEGWT	GPR EVQLEL GPR EVQLEL	QPV TPP AP QPV TPP AP	EAV RAGNS EAV RAGNS	E SLGYEGDG E SLGYEGDG
	175HARE BAB15793	943 IT TVVDF 719 IT TVVDF										
	CAB61358 AAF82398	622 TO TOTAL	A UDMCC MATE	DECOVERDED	ECEORCIVECTO	מת בשת שביות	A DOLLARGO HE	HAM KMMCDC	KHK E KCHV	TOTAL ME-ED	EOI.PIDE	DNGOTHADAK
	CAB61827 BAA13377	424 IT TVVDF 2087 RV TVADI 1730 RV TVADI										
	175HARE BAB15793 CAB61358	1052 ADLYFQD: 828 VDLHFQD: 741 VDLHFQD:	T VGVFHLRSPL	GQYKLTFDKA	REA ANEAAT	MATYNQLSYA	OKAKYHL SA	GWLETGRVAY	PTAF ASON G	SGVVGIVDYG	PRPNKSEMWD	VECYRMKDVN
	AAF82398 CAB61827	741 VDLHFQD 533 VDLHFQD 2197 TDQHFQE	CR AGVFHLQATS	GPYGLNFSEA	EAA EAQGAV	LASFPQLSAA	QQLGFHLLLM	GWLANGSTAH	PVVFPVAD: G	NGRVGVV SLG	ARKNLSERWD	AY FRVQDVA
	BAA13377 175HARE	1840 TDLHFQE			-		_		_			_
	BAB15793 CAB61358 AAF82398	938 T KVGYV0 849	SAGLF	QQLSSRPCIS	R		-TPDDLSIRG	TLFVPQNSGL	GENETLSGRD	IEHHLANVSM	FFYNDLVNGT	TLQTRLGSKL
	CAB61827 BAA13377	2307 RERNGFV	D GIST NGKLL	DVLAATANFS	TFYGMLLGYA	NATQRGLDFL	DFLDDELTYK	TLFVPVNEGF	VDNMTLSGPD	LELHASNATL	LSAN-ASQGK	LLPAHSGLSL
	175HARE BAB15793	1271 LITFS	D QLHQ-ETRFVDD PLOPTETRFV	DGRSILQWDI DGRAILOWDI	IAANGILHII FASNGIIHVI	SEPLRAPPTA SRPLKAPPAP	ATAAHSG VTLTHTG	LGTGIFCAVV LGAGIFFAII	LVTGAIAL LVTGAVAL	AAYSYFRIKQ AAYSYFRINR	RTIGFORF RTIGFOHF	DQKRTLMSWL ESEEDINVAA
	CAB61358 AAF82398	924 LITAS 752 LITAS	D PLOPTETREV D PLOPTETREV	DGRAILQWDI DGRAILQWDI	FASNGIIHVI FASNGIIHVI	SR PLKA PPA P SR PLKA PPA P	VTLTHTG VTLTHTG	LGAGIFFAII LGAGIFFAII	LVTGAVAL LVTGAVAL	AAYSYFRINR AAYSYFRINR	RTIGFQHF RTIGFQHF	ESEEDINVAA ESEEDINVAA
	CAB61827 BAA13377	2416 IISDAGPD 2059 IISDAGPD										
	175HARE BAB15793	1370 LASSSP-R 1147 LGKQQPEN 1024 LGKQQPEN	S NPLY-ESTTS	APPEPSYDPF	TDS EER		QLEGNDP	LRT L				
	CAB61358 AAF82398 CAB61827	852 LGKQQPEN 2524 SPWQ-EGT	IS NPLY-ESTTS I- PTLVSVPNPV	APPE PSYDP F FGSDTFCEP F	TDSEER DD	-SLLEEDFPD	QLEGNDP TQRILTVK	LRTL				
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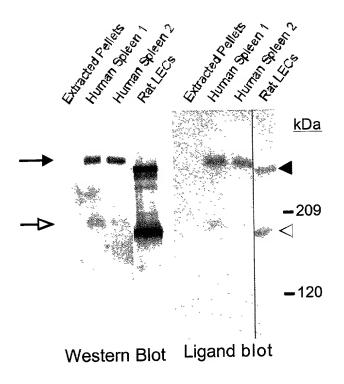
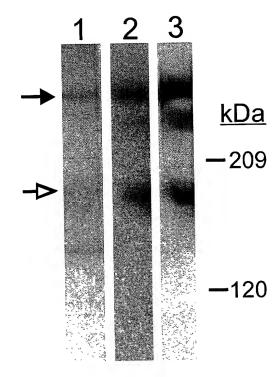
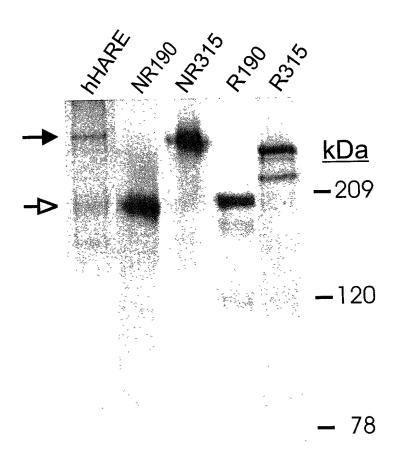
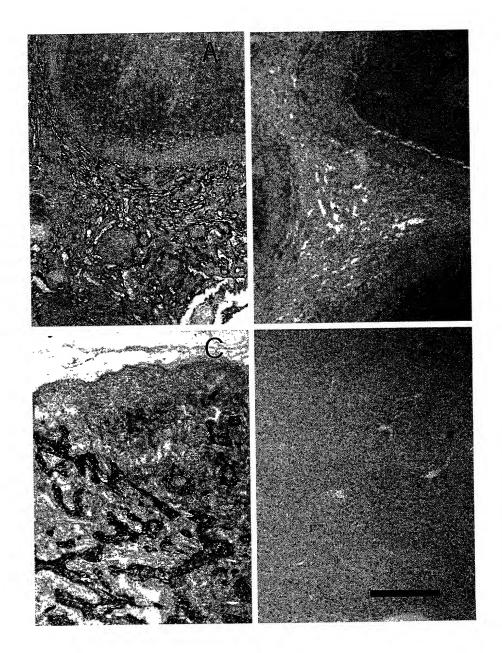


Figure 3 0



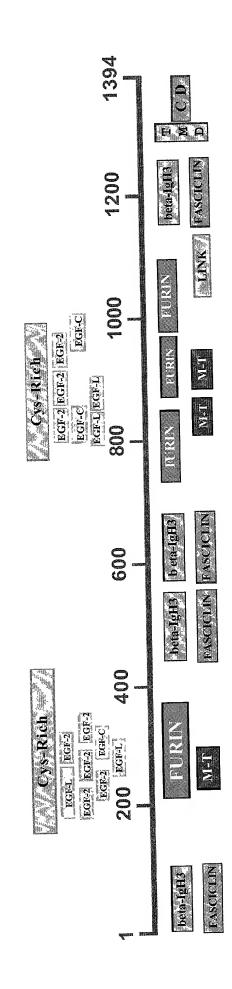




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161 T L F I G C Q P K C V R T V I T R E C C A G F F G P Q C Q P C P G N A Q N V C F 961 AGCANTGGAGGTTGCTCTGCCAAGGCTGAAGGAAGCACCCCCAGGAAGGCGAGGTGTGCACGTGCAAAGCAGGCTACACGGGTGATGGCATTGTGTGCCTGGAAATCAACCCGTGTGT321 S N G G C S A K A D C K R T T P G R R V C T C K A G Y T G D G I V C L E I N P C $^{\circ}$ 1201 GTCTGCTTAACTAAAAATGGCGGCTGTAGTGAATTTGCCATCTGCAACCACCTGGGCAAGTAGAAAGGACTTGTACTTGCAAGCCAAACTACATTGGAGATGGATTTACCTGCCGGGGC 401 V C L T K N G G C S E F A I C N H T G Q V E R T C T C K P N Y I G D G F T C R G 1321 AGCATTTATCAGGAGCTTCCCAACAACCCGAAAACTTCCCAGTATTCTTCCAGTTGCAGGAGCATTTCGTGAAAGATCTGGTCGGCCCAGGCCCCTTCACTGTTTTTGCAC
441 S I Y Q E L P K N P K T S Q Y F F Q L Q E H F V K D L V G P G P F T V F A CCTTTATCT P L S GCAGCCTTTGATGAGGAAGCTCGGGTTAAAGACTGGGACAAATACGGTTTAATGCCCCAGGTTCTTCGGTACCATGTGGTCGCCCCCCCAGCTGCTTCTGGAAAACCTGAAATTGATC
A A F D E B A R V K D W D K Y G L M P Q V L R Y H V V A C H Q L L E N L K L I 1561 TCANATGCTACTTCCCTCCAAGGAGAGCCAATAGTCATCTCCGTCTCTCAGAGCACGGTGTATATAAACAATAAGGCTAAGATCATATCCAGTGATATCATCAGTACTAATGGGATTGTT
521 S N A T S L Q G E P I V I S V S Q S T V Y I N N K A K I I S S D I I S T N G I V 1681 CATATCATAGACAAATTGCTATCTCCCAAAAATTTGCTTATCACTCCCAAAGACAACTCTGGAAGAATTCTGCAAAATCTTACGACTTTGGCAACAACAATGGCTACATCAAATTTAGC 561 H I I D K L L S P K N L L I T P K D N S G R I L Q N L T T L A T N N G Y I K F S 1801 AACTTAATACAGGACTCAGGTTTGCTGAGTGTCATCACCGATCCCATCCACCCCAGTCACTCTCTTCTCGGCCCACCGACCAAGCCCTCCATGCCCTACCTGCACAACAGGACTTC
601 N L I Q D S G L L S V I T D P I H T P V T L F W P T D Q A L H A L P A E Q Q D F 1921 CTGTTCAACCAAGACAAGACAAGGACAAGGTGATTTGAAGTTTCATGTGATACGAGGTGCCAAGGTTTTAGCTGTGGATCTTCCACATCCACTGCCTGGAAGACCCTGCAAGGT 641 L F N Q D N K D K L K E Y L K F H V I R D A K V L A V D L P T S T A W K I T L Q G 2041 TCAGAGCTGAGTGTGAAATGTGGAGCTGGCAGGGACATCGGTGACCTCTTTCTGAATGGCCAAACCTGCAGAATTGTGCAGCGGGAGCTCTTGTTTGACCTGGGTGTGGCCTACGGCATT
681 S E L S V K C G A G R D I G D L F L N G Q T C R I V Q R E L L F D L G V A Y G I 2161 GACTGTCTGCTGATTGATCCCACCCTGGGGGGCCCCTGTGACACCTTTACTACTTTCGATGCCTCGGGGGAGTGTGGGAGCTGTGTCAATACTCCCAGCTGCCCAAGGTGAGTAAACCA 2281 DAGE GTGTGAAGCAGAAGTGTCTCTACAACCTGCCCTTCAAGAGGAACCTGGAAGGCTGCCGGGAGCGGTGCAGCCTGGTGATACAGATCCCCAGGTGCTGCAACGGCTACTTCGGGCGA 761 K G V K Q K C L Y N L P F K R N L E G C R E R C S L V I Q I P R C C K G Y F G R t 2641 GGCCCCTCGTGTGACACTCAGGCAGTTTTGCCTGCAGTGTGTACGCCTCCTTGTTCTGCTCATGCCACCTGTAAGGAGAACAACACGTGTGAGTGTAACCTGGATTATGAAGGTGACGGA 881 G P S C D T Q A V L P A V C T P P C S A H A T C K E N N T C E C N L D Y E G D G 2761 ATCACATGCACAGTTGTGGATTTCTGCAAACAGGACAACGGGGGCTGTGCAAAGGTGGCCAGATGCTCCCAGAAGGGCACGAAGGTCTCCCTGCAGCTGCCAGAAGGGGATACAAAGGGGAC 921 I T C T V V D F C K Q D N G G C A K V A R C S Q K G T K V S C S C Q K G Y K G T K V S C S C Q K G Y K G T K V S C S C Q K G Y K G T K V S C S C Q K G Y K G T K V S C S C Q K G Y K G T K V S C S C Q K G Y K G T K V S C S C Q K G Y K G T K V S C S C Q K G Y K G T K V S C S C Q K G Y K G T K V S C S C Q K G Y K G T K V S C S C Q K G Y K G T K V S C S C Q K G Y K G Y K G T K V S C S C Q K G Y K G Y K G T K V S C S C Q K G Y K G Y K G T K V S C S C Q K G Y 2881 GGGCACAGCTGCACAGAGATAGACCCCTGTGCAGACGGCCTTAACGGAGGGTGTCACGAGCACGCCACCTGTAAGATGACAGGCCCGGGCAAGCACAAGTGTGAGATGACAAAGTCACTAT 961 G H S C T E I D P C A D G L N G G C H E H A T C K M T G P G K H K C E C K S H Y 3001 GTCGGAGATGGGCTGAACTGTGAGCCGGAGCAGCTGCCCATTGACCGCTGCTTACAGGACAATGGGCAGTGCCATGCAGACGCCAAATGTGTCGACCTCCACTTCCAGGATACCACTGTT
1001 V G D G L N C E P E Q L P I D R C L Q D N G Q C H A D A K C V D L H F Q D T T V 3121 GGGGTGTTCCATCTACGGTCCCACTGGGCCAGTATAAGCTGACCTTTGACAAABCCAGAAGGCCTGTGCCAACGAAGCTGCGACCATGGCAACCTACAACCAGCTCTCCTATGCCCAG
1041 G V F H L R S P L G Q Y K L T F D K A R I E A C A N E A A T M A T Y N Q L S Y A Q 3361 AGACCCAACAAGAGTGAAATGTGGGATGTCTTCTGCTATCGGATGAAGATGTGAACTGCACCTGCAAGGTGGGCTATGTGGGAGATGGCTTCTCATGCAGTGGGAACCTGCTGCAGGTC 1121 R P N K S E M W D V F C Y R M K D V N C T C K V G Y V G D G F S C S G N L L Q V TTTGTGCCACAGAACAGTGGGCTGGGGGACAATGAGACCTTGTCTGGGCGGGACATCGAGCACCTCGCCAATGTCAGCATGTTTTTCTACAATGACCTTGTCAATGGCACCCCTG F V P Q N S G L G E N E T L S G R D I E H H L A N V S M F F Y N D L V N G T T L 3601 1201 3841 ATCATTCATGTCATTTCCAGGCCTTTAAAAGCACCCCCTGCCCCCGTGACCTTGACCCACACTGGCTTGGGAGCAGGGATCTTCTTTGCCATCATCCTGGTGACTGGGGCTGTTGCCTTG
1281 I I H V I S R P L K A P P A P V T L T H T G L G A G I F F A I I L V T G A V A L 4081 TTGTATGAGAGCACAACCTCAGCTCCCCAGAACCTTCCTACGACCCCTTCACGGACTCTGAAGAACGGCAGCTTGAGGGCAATGACCCCTTGAGGACACTGTGAGGGCCTGGACGGGAG 1361 L Y E S T T S A P P E P S Y D P F T D S E E R Q L E G N D P L R T L * (1394aa) 4201 ATGCCAGCCATCACTGCCACCTGGGCCATCAACTGTGAATTCTCAGCACCAGTTGCCTTTTAGGAACGTAAAGTCCTTTAAGCACTCAGAAGCCATACCTCATCTCTCTGGCTGAT
4321 CTGGGGGTTGTTTCTGTGGGTGAGAGAGTGTGTTGCTGTGCCCACCAGTACAGCTTCCTCTCTGTGCCCTTTTGCCTTTTCTTTTTTAGCTCTTTAGCTGCTGCCCAGTACAGCTTCTCCCCAGCCCAGTACAGCCCCTAGCCCCTAGCCCTGCCAGACACAGGAACTGTGCACAATAAAGGTTTATGGAACA
4441 CTACATGATGGGTAACTGTGATCTTCTTCCCTGTTAGATTGTAAGCCTCCGTCTTTGTATCCCAGCCCCTAGCCCAGTGCCTGACACAGGAACTGTGCACAATAAAGGTTTATGGAACA 4561 GAAACAAAGTCAACAG

88 8 11

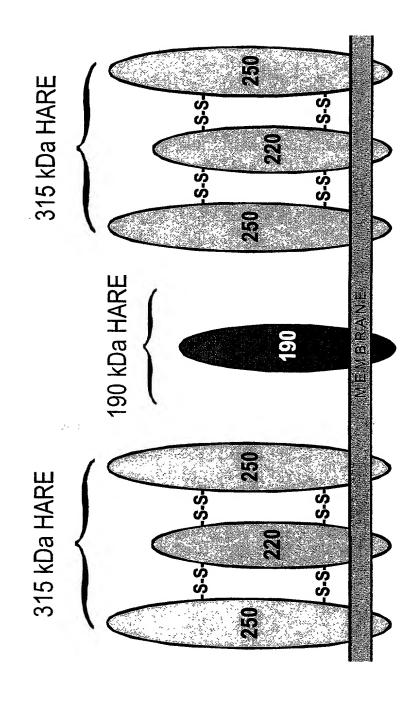
Figure 34



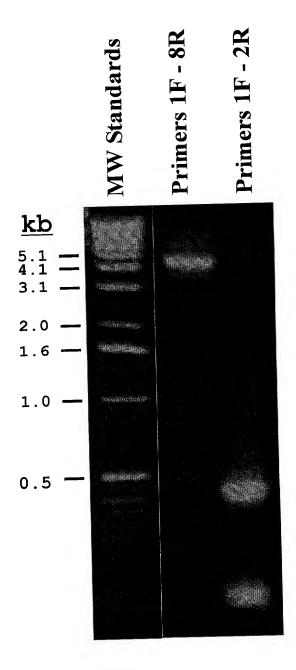
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VLRYHVVLE) ILRYHVVLG	KSLGNEKRR KPL-RETRK	A S VHGR A S VHGR	T KAGYTGDGIV V KAGYTGDGIV	SIYQELPKN SIYGELPKN	YINNKAKII FINNEAKVL	LFNQDNKDK LFNQDNKDK	ASGE GS V IPGE GS I		AR SQKGTKVS AK SQKGTQVS	VGVFHLRSI VGVFHLRSI	E KVGYVGDGFS E KAGYVGDGFS	LQTRLGSK1 LRTMLGSQ1		
NNNAIENYIREKKVLSLEED N	TIIRGR RT SSELT PFGT IIVRGE GK SQQAP PLET	FSGTA ET TEGKYGIH DO . FNGTA ET TEGKYGIH DO .	SNGG SAKAD KRTTPGRRV SNGG STKAD KRTTPGNRV	VERT T KPNYIGDGFT RG DQRI T KPDYTGDGIV RG	SNATSLQGEPIVISVSQSTV TSATTLQGEPVSISVSQDTV	TLFWPTDQALHALPAEQQDF TVFWPTDKALEALPPEQQDF	D LLIDPTLGGR DTFTTFD D LLMNPTLGGR DTFTTFD	LDQYSATGE K NTGFNGTA RDLYTPMGO L HTGFNGTA	GIT TVVDF KQDNGG AKV GIT TVVDF KQNNGG AKV	DNGQ HADAK VDLHFQDTT DNGQ HPDAS ADLYFQDTT	PRPNKSEMWDVF YRMKDVN SRANKSEMWDVF YRMKDVN	EHHLANVSMFFYNDLVNGTT EHHLTNVNVSFYNDLVNGTF	LAAYSYFRINRRTIGFQHFE LAAYSYFRLKQRTTGFQRFD	l
IQYNLANAIEAADAYTVFAP N IHYNLASAIESADAYTVFVP N	IHGLGKVLEIQKNR DNNDT I HGLEKVLEIQKNR DNNDT	GNGICLDGVNGTGV E GEG F GTASVWDGVNGTGT Q GLG F	AAGFQG <mark>NGT</mark> I TAINA EI S AAGFRG <mark>NGT</mark> V TAINA ET S	00	VLRYHVVA HQLLLENLKLI VLRYHVVG QQLLLDNLKVT	NLIQDSGLLSVITDPIHTPV KLIQDSGLLSVITDSIHTPV	QT RIVQRELLFDLGVAYGI QM RFIHRGLLFDVGVAYGI	RD QA PGGPDAP NNRGV PD QA PGGPDTP NNRGM	AHAT KE NNT E NLDYEGD VHAT TENNT V NLNYEGD	YVGDGLN EPEQLPIDR LQ YVGDGVD EPEQLPLDR LQ	PTAFASON GSGVVGIVDYG PTTYASOK GANVVGIVDYG	LFVPQNSGLGENETLSGRDI LFVPQNSGLPGNKSLSGRDI	HTGLGAGIFFAIILVTGAVA HSGLGTGIFCAVVLVTGAIA	SQQATTVTVPR
1 23	101 123	201	301	401	501 522	601 622	701	800	900	1000	1100	1200	1300	1421
hHARE rHARE	hHARE rHARE	hHARE rHARE	hhare rhare	hHARE rHARE	hHARE rHARE	hHARE rHARE	hHARE rHARE	hHARE rHARE	hHARE rHARE	hHAR rHARE	hHARE rHARE	hHARE rHARE	hHARE rHARE	rHARE

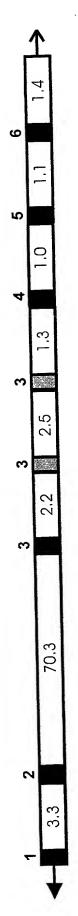
Figure 36

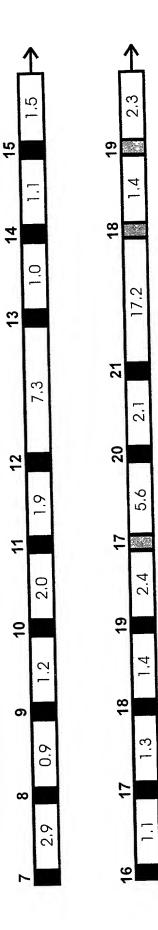


Amplification of the 1394 amino acid HARE Open Reading Frame from a human lymph node cDNA Llibrary



Schematic Organization of the Human HARE Gene on Chromosome 12 (encoding 1357 of the 1394 amino acids disclosed here)





	2.5
28	
27	3 1.4
26	.3 2.
25	
24	1.6 2.6
23	.2
22	
2	1 1.6
20	2.

